

L Number	Hits	Search Text	DB	Time stamp
1	13512	coli and (swine or pig or cattle)	USPAT; US-PGPUB; EPO; DERWENT	2003/09/30 11:06
2	4944	coli and (swine or pig or cattle) and (intestine or intestinal)	USPAT; US-PGPUB; EPO; DERWENT	2003/09/30 11:06
3	57	coli and (swine or pig or cattle) and (intestine or intestinal) and (FUT? or fucosyltransferase)	USPAT; US-PGPUB; EPO; DERWENT	2003/09/30 11:07
4	2	(coli and (swine or pig or cattle) and (intestine or intestinal) and (FUT? or fucosyltransferase)).clm.	USPAT; US-PGPUB; EPO; DERWENT	2003/09/30 11:07
5	10	coli and (swine or pig or cattle) and (intestine or intestinal) and (FUT? or fucosyltransferase) and (alteration or mutation or polymorphism).clm.	USPAT; US-PGPUB; EPO; DERWENT	2003/09/30 11:08

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<223> Description of Artificial Sequence: Primer

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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<210> 6
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<220>
<223> Description of Artificial Sequence: Primer

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<220>
<223> Description of Artificial Sequence: Primer

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<220>
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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35

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22

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<212> DNA

<213> Porcine

<220>

<221> CDS

<222> (9)..(1103)

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Met Trp Val Pro Ser Arg Arg His Leu Cys Leu Thr Phe Leu

1

5

10

cta gtc tgt gtt tta gca gca att ttc ttc ctg aac gtc tat caa gac 98

Leu Val Cys Val Leu Ala Ala Ile Phe Phe Leu Asn Val Tyr Gln Asp

15

20

25

30

ctc ttt tac agt ggc tta gac ctg ctg gcc ctg tgt cca gac cat aac 146

Leu Phe Tyr Ser Gly Leu Asp Leu Leu Ala Leu Cys Pro Asp His Asn

35

40

45

gtg gta tca tct ccc gtg gcc ata ttc tgc ctg gcg ggc acg ccg gta 194

Val Val Ser Ser Pro Val Ala Ile Phe Cys Leu Ala Gly Thr Pro Val

50

55

60

cac ccc aac gcc tcc gat tcc tgt ccc aag cat cct gcc tcc ttt tcc His Pro Asn Ala Ser Asp Ser Cys Pro Lys His Pro Ala Ser Phe Ser 65 70 75	242
ggg acc tgg act att tac ccg gat ggc cgg ttt ggg aac cag atg gga Gly Thr Trp Thr Ile Tyr Pro Asp Gly Arg Phe Gly Asn Gln Met Gly 80 85 90	290
cag tat gcc acg ctg ctg gcc ctg gcg cag ctc aac ggc cgc cag gcc Gln Tyr Ala Thr Leu Leu Ala Leu Ala Gln Leu Asn Gly Arg Gln Ala 95 100 105 110	338
ttc atc cag cct gcc atg cac gcc gtc ctg gcc ccc gtg ttc cgc atc Phe Ile Gln Pro Ala Met His Ala Val Leu Ala Pro Val Phe Arg Ile 115 120 125	386
acg ctg cct gtc ctg gcg ccc gag gta gac agg cac gct cct tgg cgg Thr Leu Pro Val Leu Ala Pro Glu Val Asp Arg His Ala Pro Trp Arg 130 135 140	434
gag ctg gag ctt cac gac tgg atg tcc gag gat tat gcc cac tta aag Glu Leu Glu Leu His Asp Trp Met Ser Glu Asp Tyr Ala His Leu Lys 145 150 155	482
gag ccc tgg ctg aag ctc acc ggc ttc ccc tgc tcc tgg acc ttc ttc Glu Pro Trp Leu Lys Leu Thr Gly Phe Pro Cys Ser Trp Thr Phe Phe 160 165 170	530
cac cac ctc cgg gag cag atc cgc agc gag ttc acc ctg cac gac cac His His Leu Arg Glu Gln Ile Arg Ser Glu Phe Thr Leu His Asp His 175 180 185 190	578
ctt cgg caa gag gcc cag ggg gta ctg agt cag ttc cgt cta ccc cgc Leu Arg Gln Glu Ala Gln Gly Val Leu Ser Gln Phe Arg Leu Pro Arg 195 200 205	626
aca ggg gac cgc ccc agc acc ttc gtg ggg gtc cac gtg cgc cgc ggg Thr Gly Asp Arg Pro Ser Thr Phe Val Gly Val His Val Arg Arg Gly 210 215 220	674
gac tat ctg cgt gtg atg ccc aag cgc tgg aag ggg gtg gtg ggt gac Asp Tyr Leu Arg Val Met Pro Lys Arg Trp Lys Gly Val Val Gly Asp 225 230 235	722
ggc cgt tac ctc cag cag gct atg gac tgg ttc cgg gcc cga tac gaa Gly Arg Tyr Leu Gln Gln Ala Met Asp Trp Phe Arg Ala Arg Tyr Glu 240 245 250	770
gcc ccc gtc ttt gtg gtc acc agc aac ggc atg gag tgg tgc cgg aag Ala Pro Val Phe Val Val Thr Ser Asn Gly Met Glu Trp Cys Arg Lys 255 260 265 270	818
aac atc gac acc tcc cgg ggg gac gtg atc ttt gct ggc gat ggg cgg Asn Ile Asp Thr Ser Arg Gly Asp Val Ile Phe Ala Gly Asp Gly Arg 275 280 285	866

gag gcc gcg ccc gcc agg gac ttt gcg ctg ctg gtg cag tgc aac cac 914
 Glu Ala Ala Pro Ala Arg Asp Phe Ala Leu Leu Val Gln Cys Asn His
 290 295 300

acc atc atg acc att ggc acc ttc ggc ttc tgg gcc gcc tac ctg gct 962
 Thr Ile Met Thr Ile Gly Thr Phe Gly Phe Trp Ala Ala Tyr Leu Ala
 305 310 315

ggt gga gat acc atc tac ttg gct aac ttc acc ctg ccc act tcc agc 1010
 Gly Gly Asp Thr Ile Tyr Leu Ala Asn Phe Thr Leu Pro Thr Ser Ser
 320 325 330

ttc ctg aag atc ttt aaa ccc gag gct gcc ttc ctg ccc gag tgg gtg 1058
 Phe Leu Lys Ile Phe Lys Pro Glu Ala Ala Phe Leu Pro Glu Trp Val
 335 340 345 350

ggc att aat gca gac ttg tct cca ctc cag atg ttg gct ggg cct 1103
 Gly Ile Asn Ala Asp Leu Ser Pro Leu Gln Met Leu Ala Gly Pro
 355 360 365

tgaaccagcc aggagccttt ctggaatagc ctcggtcaac ccagggccag cgttatgggt 1163

ctccggaagc ccgagtaact tccggagatg ctggtggtcc tgtagcaggc tggacactta 1223

tttcaagagt gattctaatt ggctggactc agaggaaacc ctgcag 1269

<210> 13
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<400> 13
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Cys Val Leu Ala Ala Ile Phe Phe Leu Asn Val Tyr Gln Asp Leu Phe
 20 25 30

Tyr Ser Gly Leu Asp Leu Leu Ala Leu Cys Pro Asp His Asn Val Val
 35 40 45

Ser Ser Pro Val Ala Ile Phe Cys Leu Ala Gly Thr Pro Val His Pro
 50 55 60

Asn Ala Ser Asp Ser Cys Pro Lys His Pro Ala Ser Phe Ser Gly Thr
 65 70 75 80

Trp Thr Ile Tyr Pro Asp Gly Arg Phe Gly Asn Gln Met Gly Gln Tyr
 85 90 95

Ala Thr Leu Leu Ala Leu Ala Gln Leu Asn Gly Arg Gln Ala Phe Ile
 100 105 110

Gln Pro Ala Met His Ala Val Leu Ala Pro Val Phe Arg Ile Thr Leu
 115 120 125

Pro Val Leu Ala Pro Glu Val Asp Arg His Ala Pro Trp Arg Glu Leu
 130 135 140

Glu Leu His Asp Trp Met Ser Glu Asp Tyr Ala His Leu Lys Glu Pro
 145 150 155 160

Trp Leu Lys Leu Thr Gly Phe Pro Cys Ser Trp Thr Phe Phe His His
 165 170 175

Leu Arg Glu Gln Ile Arg Ser Glu Phe Thr Leu His Asp His Leu Arg
 180 185 190

Gln Glu Ala Gln Gly Val Leu Ser Gln Phe Arg Leu Pro Arg Thr Gly
 195 200 205

Asp Arg Pro Ser Thr Phe Val Gly Val His Val Arg Arg Gly Asp Tyr
 210 215 220

Leu Arg Val Met Pro Lys Arg Trp Lys Gly Val Val Gly Asp Gly Arg
 225 230 235 240

Tyr Leu Gln Gln Ala Met Asp Trp Phe Arg Ala Arg Tyr Glu Ala Pro
 245 250 255

Val Phe Val Val Thr Ser Asn Gly Met Glu Trp Cys Arg Lys Asn Ile
 260 265 270

Asp Thr Ser Arg Gly Asp Val Ile Phe Ala Gly Asp Gly Arg Glu Ala
 275 280 285

Ala Pro Ala Arg Asp Phe Ala Leu Leu Val Gln Cys Asn His Thr Ile
 290 295 300

Met Thr Ile Gly Thr Phe Gly Phe Trp Ala Ala Tyr Leu Ala Gly Gly
 305 310 315 320

Asp Thr Ile Tyr Leu Ala Asn Phe Thr Leu Pro Thr Ser Ser Phe Leu
 325 330 335

Lys Ile Phe Lys Pro Glu Ala Ala Phe Leu Pro Glu Trp Val Gly Ile
 340 345 350

Asn Ala Asp Leu Ser Pro Leu Gln Met Leu Ala Gly Pro
 355 360 365